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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/464,099A

DATE: 07/19/2001

TIME: 15:37:51

Input Set : A:\MOBT175-2.ST25.txt

Output Set: N:\CRF3\07192001\I464099A.raw

PS

3 <110> APPLICANT: Barry, Gerard F.
 4 Kishore, Ganesh M.
 5 Padgett, Stephen R.
 6 Stallings, William C.
 8 <120> TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE
 SYNTHASES

ENTERED

10 <130> FILE REFERENCE: 11899.0175.CNUS01 MOBT:175-2
 12 <140> CURRENT APPLICATION NUMBER: 09/464,099A
 13 <141> CURRENT FILING DATE: 1999-12-16
 15 <150> PRIOR APPLICATION NUMBER: US 09/137,440
 16 <151> PRIOR FILING DATE: 1998-08-20
 18 <150> PRIOR APPLICATION NUMBER: US 08/833,485
 19 <151> PRIOR FILING DATE: 1997-04-07
 21 <150> PRIOR APPLICATION NUMBER: US 08/306,063
 22 <151> PRIOR FILING DATE: 1994-09-13
 24 <150> PRIOR APPLICATION NUMBER: US 07/749,611
 25 <151> PRIOR FILING DATE: 1991-08-28
 27 <150> PRIOR APPLICATION NUMBER: US 07/576,537
 28 <151> PRIOR FILING DATE: 1990-08-31
 30 <160> NUMBER OF SEQ ID NOS: 70
 32 <170> SOFTWARE: PatentIn version 3.0
 34 <210> SEQ ID NO: 1
 35 <211> LENGTH: 597
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Figwort mosaic virus
 39 <400> SEQUENCE: 1
 40 tcatacaaaat atttagcagc attccagatt gggttcaatc aacaaggtag gagccatattc 60
 42 actttattca aattggtatc gccaaaacca agaaggaact cccatcctca aagggtttgta 120
 44 aggaagaatt ctgagtcaca agcctcaaca aggtcagggt acagagtctc caaaccatta 180
 46 gccaaaagct acaggagatc aatgaagaat ctccaatcaa agtaaaactac tgttccagca 240
 48 catgcatcat ggtcagtaag ttccagaaaa agacatccac cgaagactta aagttagtgg 300
 50 gcatctttga aagtaattct gtcaacatcg agcagctggc ttgtggggac cagacaaaaa 360
 52 aggaatgggt cagaattggt aggcgcacct accaaaagca tctttgcctt tattgcaaag 420
 54 ataaagcaga ttcctctagt acaagtgggg aacaaaataa cgtggaaaag agctgtcctg 480
 56 acagccact cactaatgag tatgacgaac gcagtgcga ccacaaaaga attccctcta 540
 58 tataagaagg cattcattcc catttgaagg atcatcagat actaaccaat atttctc 597
 61 <210> SEQ ID NO: 2
 62 <211> LENGTH: 1982
 63 <212> TYPE: DNA
 64 <213> ORGANISM: Agrobacterium sp.
 66 <220> FEATURE:
 67 <221> NAME/KEY: CDS
 68 <222> LOCATION: (62)..(1426)
 70 <400> SEQUENCE: 2
 71 aagcccgctg tctctccggc gctccgcccg gagagccgtg gatagattaa ggaagacgcc 60
 73 c atg tcg cac ggt gca agc agc cgg ccc gca acc gcc cgc aaa tcc tct 109
 74 Met Ser His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser
 75 1 5 10 15

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77 ggc ctt tcc gga acc gtc cgc att ccc ggc gac aag tcg atc tcc cac      157
78 Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser His
79          20          25          30
81 cgg tcc ttc atg ttc ggc ggt ctc gcg agc ggt gaa acg cgc atc acc      205
82 Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
83          35          40          45
85 ggc ctt ctg gaa ggc gag gac gtc atc aat acg ggc aag gcc atg cag      253
86 Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met Gln
87          50          55          60
89 gcc atg ggc gcc agg atc cgt aag gaa ggc gac acc tgg atc atc gat      301
90 Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp
91 65          70          75          80
93 ggc gtc ggc aat ggc ggc ctc ctg gcg cct gag gcg ccg ctc gat ttc      349
94 Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe
95          85          90          95
97 ggc aat gcc gcc acg ggc tgc cgc ctg acc atg ggc ctc gtc ggg gtc      397
98 Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly Val
99          100          105          110
101 tac gat ttc gac agc acc ttc atc ggc gac gcc tcg ctc aca aag cgc      445
102 Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys Arg
103          115          120          125
105 ccg atg ggc cgc gtg ttg aac ccg ctg cgc gaa atg ggc gtg cag gtg      493
106 Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
107          130          135          140
109 aaa tcg gaa gac ggt gac cgt ctt ccc gtt acc ttg cgc ggg ccg aag      541
110 Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro Lys
111 145          150          155          160
113 acg ccg acg ccg atc acc tac cgc gtg ccg atg gcc tcc gca cag gtg      589
114 Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
115          165          170          175
117 aag tcc gcc gtg ctg ctc gcc ggc ctc aac acg ccc ggc atc acg acg      637
118 Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr Thr
119          180          185          190
121 gtc atc gag ccg atc atg acg cgc gat cat acg gaa aag atg ctg cag      685
122 Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
123          195          200          205
125 ggc ttt ggc gcc aac ctt acc gtc gag acg gat gcg gac ggc gtg cgc      733
126 Gly Phe Gly Ala Asn Leu Thr Val Glu Thr Asp Ala Asp Gly Val Arg
127          210          215          220
129 acc atc cgc ctg gaa ggc cgc ggc aag ctc acc ggc caa gtc atc gac      781
130 Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile Asp
131 225          230          235          240
133 gtg ccg ggc gac ccg tcc tcg acg gcc ttc ccg ctg gtt gcg gcc ctg      829
134 Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
135          245          250          255
137 ctt gtt ccg ggc tcc gac gtc acc atc ctc aac gtg ctg atg aac ccc      877
138 Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn Pro
139          260          265          270
141 acc cgc acc ggc ctc atc ctg acg ctg cag gaa atg ggc gcc gac atc      925

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142 Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
143      275      280      285
145 gaa gtc atc aac ccg cgc ctt gcc ggc ggc gaa gac gtg gcg gac ctg      973
146 Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
147      290      295      300
149 cgc gtt cgc tcc tcc acg ctg aag ggc gtc acg gtg ccg gaa gac cgc      1021
150 Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp Arg
151 305      310      315      320
153 gcg cct tcg atg atc gac gaa tat ccg att ctc gct gtc gcc gcc gcc      1069
154 Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala Ala
155      325      330      335
157 ttc gcg gaa ggg gcg acc gtg atg aac ggt ctg gaa gaa ctc cgc gtc      1117
158 Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg Val
159      340      345      350
161 aag gaa agc gac cgc ctc tcg gcc gtc gcc aat ggc ctc aag ctc aat      1165
162 Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu Asn
163      355      360      365
165 ggc gtg gat tgc gat gag ggc gag acg tcg ctc gtc gtg cgc ggc cgc      1213
166 Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly Arg
167      370      375      380
169 cct gac ggc aag ggg ctc ggc aac gcc tcg ggc gcc gcc gtc gcc acc      1261
170 Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr
171 385      390      395      400
173 cat ctc gat cac cgc atc gcc atg agc ttc ctc gtc atg ggc ctc gtg      1309
174 His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
175      405      410      415
177 tcg gaa aac cct gtc acg gtg gac gat gcc acg atg atc gcc acg agc      1357
178 Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser
179      420      425      430
181 ttc ccg gag ttc atg gac ctg atg gcc ggc ctg ggc gcg aag atc gaa      1405
182 Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu
183      435      440      445
185 ctc tcc gat acg aag gct gcc tgatgacctt cacaatcgcc atcgatggtc      1456
186 Leu Ser Asp Thr Lys Ala Ala
187      450      455
189 ccgctgcggc cggcaagggg acgctctcgc gccgtatcgc ggaggtctat ggctttcatc      1516
191 atctcgatac gggcctgacc tatcgcgcca cggccaaagc gctgctcgat cgcggcctgt      1576
193 cgcttgatga cgaggcgggt gcggccgatg tcgccgcaa tctcgatctt gccgggctcg      1636
195 accggtcggg gctgtcggcc catgccatcg gcgaggcggc ttcgaagatc gcggtcatgc      1696
197 cctcgggtgc gcgggcgctg gtcgaggcgc agcgagctt tgcggcgctg gagccgggca      1756
199 ccgtgctgga tggacgcgat atcggcacgg tggctctgcc ggatgcgccg gtgaagctct      1816
201 atgtcaccgc gtcaccggaa gtgcgcgcga aacgccgcta tgacgaaatc ctcggcaatg      1876
203 gcgggttggc cgattacggg acgatcctcg aggatatccg ccgccgcgac gagcgggaca      1936
205 tgggtcgggc ggacagtcct ttgaagcccg ccgacgatgc gcactt      1982
208 <210> SEQ ID NO: 3
209 <211> LENGTH: 455
210 <212> TYPE: PRT
211 <213> ORGANISM: Agrobacterium sp.
213 <400> SEQUENCE: 3

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215 Met Ser His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser
216 1 5 10 15
219 Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser His
220 20 25 30
223 Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
224 35 40 45
227 Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met Gln
228 50 55 60
231 Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp
232 65 70 75 80
235 Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe
236 85 90 95
239 Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly Val
240 100 105 110
243 Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys Arg
244 115 120 125
247 Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
248 130 135 140
251 Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro Lys
252 145 150 155 160
255 Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
256 165 170 175
259 Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr Thr
260 180 185 190
263 Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
264 195 200 205
267 Gly Phe Gly Ala Asn Leu Thr Val Glu Thr Asp Ala Asp Gly Val Arg
268 210 215 220
271 Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile Asp
272 225 230 235 240
275 Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
276 245 250 255
279 Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn Pro
280 260 265 270
283 Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
284 275 280 285
287 Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
288 290 295 300
291 Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp Arg
292 305 310 315 320
295 Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala Ala
296 325 330 335
299 Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg Val
300 340 345 350
303 Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu Asn
304 355 360 365
307 Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly Arg
308 370 375 380
311 Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr

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Output Set: N:\CRF3\07192001\I464099A.raw

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312 385          390          395          400
315 His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
316          405          410          415
319 Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser
320          420          425          430
323 Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu
324          435          440          445
327 Leu Ser Asp Thr Lys Ala Ala
328          450          455
331 <210> SEQ ID NO: 4
332 <211> LENGTH: 1673
333 <212> TYPE: DNA
334 <213> ORGANISM: Agrobacterium sp.
336 <220> FEATURE:
337 <221> NAME/KEY: CDS
338 <222> LOCATION: (86)..(1432)
340 <400> SEQUENCE: 4
341 gtagccacac ataattacta tagctaggaa gcccgctatc tctcaatccc gcgtgatcgc 60
343 gccaaaaatgt gactgtgaaa aatcc atg tcc cat tct gca tcc ccg aaa cca 112
344          Met Ser His Ser Ala Ser Pro Lys Pro
345          1          5
347 gca acc gcc cgc cgc tcg gag gca ctc acg ggc gaa atc cgc att ccg 160
348 Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg Ile Pro
349 10          15          20          25
351 ggc gac aag tcc atc tcg cat cgc tcc ttc atg ttt ggc ggt ctc gca 208
352 Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu Ala
353          30          35          40
355 tcg ggc gaa acc cgc atc acc ggc ctt ctg gaa ggc gag gac gtc atc 256
356 Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp Val Ile
357          45          50          55
359 aat aca ggc cgc gcc atg cag gcc atg ggc gcg aaa atc cgt aaa gag 304
360 Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg Lys Glu
361          60          65          70
363 ggc gat gtc tgg atc atc aac ggc gtc ggc aat ggc tgc ctg ttg cag 352
364 Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu Leu Gln
365          75          80          85
367 ccc gaa gct gcg ctc gat ttc ggc aat gcc gga acc ggc gcg cgc ctc 400
368 Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala Arg Leu
369 90          95          100          105
371 acc atg ggc ctt gtc ggc acc tat gac atg aag acc tcc ttt atc ggc 448
372 Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe Ile Gly
373          110          115          120
375 gac gcc tcg ctg tcg aag cgc ccg atg ggc cgc gtg ctg aac ccg ttg 496
376 Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn Pro Leu
377          125          130          135
379 cgc gaa atg ggc gtt cag gtg gaa gca gcc gat ggc gac cgc atg ccg 544
380 Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg Met Pro
381          140          145          150
383 ctg acg ctg atc ggc ccg aag acg gcc aat ccg atc acc tat cgc gtg 592

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:1278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1443 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:1550 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:1569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:2605 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54